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<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION EFFICIENCY

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<170> PatentIn version 3.1

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635

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gcc tac act tgt ccc tac cag aac gtc atg gac Ggc gta ctg aac tat			816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr			
260	265	270	
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc			864
Pro Ile Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser			
275	280	285	
atg gac gac ctc tac aac atg atc aac acc gtc aaaa tcc gac tgt cca			912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro			
290	295	300	
gac tca aca ctc ctg ggc aca ttc gtc gag aac Cac gac aac cca cgg			960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg			
305	310	315	320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca			1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala			
325	330	335	
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa			1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu			
340	345	350	
cag cac tac gcc ggc gga aac gac ccc gcg aac Cgc gaa gca acc tgg			1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp			
355	360	365	
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc			1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser			
370	375	380	
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg			1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val			
385	390	395	400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg			1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met			

405	410	415	
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag			
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys			1296
420	425	430	
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac			
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr			1344
435	440	445	
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg			
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr			1392
450	455	460	
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct			
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro			1440
465	470	475	480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt			
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser			1488
485	490	495	
agc tcg tga			1497
Ser Ser			

<210> 11
 <211> 498
 <212> PRT
 <213> Aspergillus niger

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala			
35	40	45	
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Thr Trp Gln Gly			
50	55	60	
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile			
65	70	75	80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly			
85	90	95	
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu			
100	105	110	
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His			
115	120	125	
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly			
130	135	140	
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe			
145	150	155	160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu			
165	170	175	
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser			
180	185	190	
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr			
195	200	205	
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg			
210	215	220	
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn			
225	230	235	240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270
 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 290 295 300
 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335
 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 415
 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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 Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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 Ser Ser

<210> 12
 <211> 3697
 <212> DNA
 <213> Aspergillus niger

<400> 12

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agtttgtgtc tgtataatat atacatgtaa	gatacatgag cttcggtgat ataatacaga	180
agtaccatcac agtaccgcgt tataaaaaca	cattaatccg gatcctttcc tataatagac	240
tagcgtgctt ggcatttaggg ttcaaaaaac aatcgaagag	tataaggaa tgacagcagt	300
aacgactcca actgtacgcc tccggtagt agaccgagca	gccgagccag ctcagcgcct	360
aaaacgcctt atacaattaa gcagttaaag aagttagaat	ctacgcttaa aaagctactt	420
aaaaatcgat ctcgcagtcc cgattcgctt atcaaaacca	gtttaatca actgattaaa	480
ggtgccgAAC gagctataaa tgatataaca atattaaagc	attaattaga gcaatatcag	540
gcccgcacg aaaggcaact taaaaagcga aagcgtctta	ctaaacagat tactttgaa	600
aaaggcacat cagtattaa agccgaaatc cttattaagc	gccgaaatca ggcagataaa	660
gccatacagg cagatagacc tctacctatt aaatcggctt	ctaggcgcgc tccatctaaa	720
tgttctggct gtgggttaca gggcataaa attacgcact	acccgaaatcg atagaactac	780
tcatttttat atagaagtca gaattcatgg tggtttgatc	attttaaatt ttttatatggc	840
gggtgggggg caactcgctt gcgcgggcaa ctcgcttacc	gattacgtta gggctgatat	900
ttacgtaaaa atcgtcaagg gatgcaagac caaagtagta	aaaccccgga gtcaacagca	960

tccaa	gccc	ag	tcc	ttcac	ggagaa	accc	cag	gtcc	ac	atc	acg	agcg	aagg	acc	acc	1020
tct	agg	cat	c	gac	ccac	ca	tt	aa	tt	ac	ac	gg	aa	cc	cc	1080
gtc	gg	cc	cc	gt	ttt	ca	tt	aa	tt	ac	ac	gg	cc	cc	cc	1140
cag	at	gt	gact	gg	gg	aa	tt	aa	tt	ca	ac	cc	ac	aa	at	1200
cgt	cc	cc	gg	gt	ct	tc	tt	aa	tt	ca	ac	cc	ac	at	at	1260
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tg	ta	aa	ct	gt	at	aa	tt	tt	tc	tt	tc	tt	ca	aa	gg	aa
tg	ta	aa	ct	gt	at	aa	tt	tt	tc	tt	tc	tt	ca	aa	gg	1680
ta	aa	tt	tt	cc	cc	aa	tt	tt	tc	tt	tc	tt	ca	aa	gg	1740
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gg	ct	ac	tt	cc	cc	aa	tt	tt	tc	tt	tc	tt	tc	cc	at	1920
at	ca	aa	tt	tt	cc	aa	tt	tt	tc	tt	tc	tt	tc	cc	at	1980
gat	gac	tt	tt	cc	cc	aa	tt	tt	tc	tt	tc	tt	tc	cc	at	2040
gt	gg	tt	tt	cc	cc	aa	tt	tt	tc	tt	tc	tt	tc	cc	at	2100
tc	ag	ta	ct	gt	gg	tt	tc	tt	tc	tt	tc	tt	tc	cc	at	2160
gt	gt	tt	ta	cc	tt	cc	aa	tt	tc	tt	tc	tt	tc	cc	at	2220
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gt	ta	ct	at	tt	cc	aa	tt	tc	tt	tc	tt	tc	tt	cc	at	2940
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cc	cc	cc	cc	cc	cc	aa	tt	tc	tt	tc	tt	tc	tt	cc	at	3420
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cc	cc	cc	cc	cc	cc	aa	tt	tc	tt	tc	tt	tc	tt	cc	at	3540
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<213> *Aspergillus niger*

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Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr	
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ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg	144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala	
35 40 45	
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc	192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly	
50 55 60	
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc	240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile	
65 70 75 80	
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga	288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly	
85 90 95	
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa	336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu	
100 105 110	
aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat	384
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His	
115 120 125	
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc	432
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly	
130 135 140	
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc	480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe	
145 150 155 160	
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa	528
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu	
165 170 175	
gat cag act cag gag gat tgc tgg cta gga gat aac act gtc tcc	576
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser	
180 185 190	
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac	624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr	
195 200 205	
gac tgg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt	672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg	
210 215 220	
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Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn	
225 230 235 240	
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg	768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro	
245 250 255	
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat	816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr	
260 265 270	
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc	864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser	
275 280 285	
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca	912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro	

290	295	300	
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cg			960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg			
305	310	315	320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca			1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala			
325	330	335	
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa			1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu			
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cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg			1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp			
355	360	365	
ctc tcg ggc tac ccg acc gac gag ctg tac aag tta att gcc tcc			1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser			
370	375	380	
gcg aac gca atc cgg aac tat gcc att agc aac gat aca gga ttc gtg			1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val			
385	390	395	400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg			1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met			
405	410	415	
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag			1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys			
420	425	430	
ggg gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac			1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr			
435	440	445	
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg			1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr			
450	455	460	
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct			1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro			
465	470	475	480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt			1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser			
485	490	495	
agc tcg tga			1497
Ser Ser			

<210> 14
<211> 498
<212> PRT
<213> Aspergillus niger

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35 40 45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
50 55 60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile

65 70 75 80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 85 90 95
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 100 105 110
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 115 120 125
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 130 135 140
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 145 150 155 160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 165 170 175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 180 185 190
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 195 200 205
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 210 215 220
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
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Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
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Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 415
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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 485 490 495
Ser Ser

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<212> DNA
<213> *Aspergillus niger*

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 tttaaaataa ccatatacta agtgaatca ccagtcgacg gactccg cat cgacagtgtc 1980
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 aqtcggatgg gactgttact tggaaaagtg attcgaatcg ggagtat acg gtgccggagt 3120

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tagccagtgg	gcttgaagaa	aagtctcctg	ggtctctgg	ttgagtagcc	atgttaagat	3420
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<210> 16
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<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(1518)

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1																15
aag	ctg	gcc	ctc	ggg	ctg	tcg	gct	gca	gaa	tgg	cgc	act	cag	tcg	att	96
Lys	Leu	Ala	Leu	Gly	Leu	Ser	Ala	Ala	Glu	Trp	Arg	Thr	Gln	Ser	Ile	
																30
tac	tcc	cta	ttg	acg	gat	cggt	ttc	ggt	agg	acg	gac	aat	tcg	acg	aca	144
Tyr	Phe	Leu	Leu	Thr	Asp	Arg	Phe	Gly	Arg	Thr	Asp	Asn	Ser	Thr	Thr	
																45
gct	aca	tgc	gat	acg	ggt	gac	caa	atc	tat	tgt	ggt	ggc	agt	tgg	caa	192
Ala	Thr	Cys	Asp	Thr	Gly	Asp	Gln	Ile	Tyr	Cys	Gly	Gly	Ser	Trp	Gln	
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gga	atc	atc	aac	cat	ctg	gat	tat	atc	cag	ggc	atg	gga	tcc	acg	gcc	240
Gly	Ile	Ile	Asn	His	Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	
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atc	tgg	atc	tcg	cct	atc	act	gaa	cag	ctg	ccc	cag	gat	act	gct	gat	288
Ile	Trp	Ile	Ser	Pro	Ile	Thr	Glu	Gln	Leu	Pro	Gln	Asp	Thr	Ala	Asp	
																95
ggt	gaa	gct	tac	cat	gga	tat	tgg	cag	cag	aag	ata	tac	gac	gtg	aac	336
Gly	Glu	Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Lys	Ile	Tyr	Asp	Val	Asn	
																110
tcc	aac	ttc	ggc	act	gca	gat	gac	ctc	aag	tcc	ctc	tca	gat	gcg	ctt	384
Ser	Asn	Phe	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ser	Leu	Ser	Asp	Ala	Leu	
																125
cat	gcc	cgc	gga	atg	tac	ctc	atg	gtg	gac	gtc	gtc	cct	aac	cac	atg	432
His	Ala	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Pro	Asn	His	Met	
																140
ggc	tac	gcc	ggc	aac	ggc	aac	gat	gta	gac	tac	agc	gtc	ttc	gac	ccc	480
Gly	Tyr	Ala	Gly	Asn	Gly	Asn	Asp	Val	Asp	Tyr	Ser	Val	Phe	Asp	Pro	
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tcc	gat	tcc	tcc	tcc	tac	tcc	cac	cca	tac	tgc	ctg	atc	aca	gat	tgg	528
Phe	Asp	Ser	Ser	Tyr	Phe	His	Pro	Tyr	Cys	Leu	Ile	Thr	Asp	Trp		
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gac	aac	ttg	acc	atg	gtc	caa	gat	tgt	tgg	gag	ggt	gac	acc	atc	gta	576
Asp	Asn	Leu	Thr	Met	Val	Gln	Asp	Cys	Trp	Glu	Gly	Asp	Thr	Ile	Val	
																190
tct	ctg	cca	gac	cta	aac	acc	acc	gaa	act	gcc	gtg	aga	aca	atc	tgg	624

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500 505

<210> 17
<211> 505
<212> PRT
<213> Aspergillus niger

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Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
35 40 45
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
50 55 60
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65 70 75 80
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp
85 90 95
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn
100 105 110
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
115 120 125
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
130 135 140
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
145 150 155 160
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
165 170 175
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
180 185 190
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
195 200 205
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
210 215 220
Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
225 230 235 240
Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
245 250 255
Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
260 265 270
Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
275 280 285
Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
290 295 300
Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
305 310 315 320
Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
325 330 335
Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
340 345 350
Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
355 360 365
Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala

370	375	380
Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr		
385	390	395
		400

Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala	405	410	415	
Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn	420	425	430	
Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly	435	440	445	
Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val	450	455	460	
Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu	465	470	475	480
Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys	485	490	495	
Gly Gly Ser Gly Arg Leu Tyr Val Glu	500	505		

<210> 18
 <211> 2935
 <212> DNA
 <213> *Penicillium chrysogenum*

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atccctttc ctttcgcaga tgcgtgcgc caaaatccag agagcacgt ccaccggca	1860
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gtgtacgatc cttccaaaata tccgaatcct tgcgtgcct cgtcaatctca atctttgggta	1980
caatgatact gactgattcg cagcgctca atggcattat cgtatctac aggtatcg	2040
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<210> 19
 <211> 1977
 <212> DNA
 <213> *Penicillium chrysogenum*

<220>
 <221> CDS
 <222> (1)..(1977)

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gag ctc gag acc agc ttc aaa tca gtc aaa gat gcg gtg ctg ttt	96
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe	
20 25 30	
gtt ata gat att agc agt tcg atg ctc acg cct cgt cca tcg cct gat	144
Ala Ile Asp Ile Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp	
35 40 45	
cct aag aaa cat gga gac gaa tca ccc gcg tct gca gct ttg aag tgt	192
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys	
50 55 60	
gca tac cat ctg atg caa caa cgc atc atc tcc aac cct cat gac atg	240
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met	
65 70 75 80	
att ggc gtt ttg ctt tac gga acg caa tct tcc aag ttc tat gat gaa	288
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu	
85 90 95	
aat gag gat gac cgt gga gat ctc tca tat cct cac tgt tat ctg tac	336
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr	
100 105 110	
acg gat ctt gat gtt cca tca gcc cag gaa gtc aag caa ctg cgg tcc	384
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser	
115 120 125	

ctc gca tct cca gca gat gct gat gat gac gta ctg caa gtt ttg gag	432
Leu Ala Ser Pro Ala Asp Ala Asp Asp Asp Val Leu Gln Val Leu Glu	
130 135 140	
cca tca aag gag cca gcc tcc atg gcc aac atg ctt ttc tgc gcc aac	480
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn	
145 150 155 160	
caa atc ttt acc tca aaa gct cca aac ttt gct tct cga cgc ctg ttt	528
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe	
165 170 175	
gtc gtg acc gac aac gat aat ccc cac gca gac aac aaa gga atg cg	576
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg	
180 185 190	
tct gct gca aca gtt cgt gcg agg gac ttg tac gat ctt ggt gtc aat	624
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn	
195 200 205	
atc gag ttg ttt ccc ata tct caa cca gac cac gaa ttc gac acc tct	672
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser	
210 215 220	
aaa ttc tac gac gac att atc tac aaa aca tcg ccc agt gat gga gat	720
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp	
225 230 235 240	
gcc cct gca tac cta cag ccg gat acc aac aca tca aca gct aaa ggc	768
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly	
245 250 255	
gat gga ctt tca ttg ctc aat tct ctg ttg tcg agc atc aac tca cga	816
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg	
260 265 270	
tct gtc ccc cgc cga tcg ctg ttc tca aat gtg cca ctt gag atc gga	864
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly	
275 280 285	
cct aat ttc aaa ata tcc gtc aat gga tat ttg ctt ctc aag aaa caa	912
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Lys Lys Gln	
290 295 300	
gag cct gca agg agt tgc ttc gtc tgg caa gga ggc gag act gct cag	960
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Glu Thr Ala Gln	
305 310 315 320	
att gcc aaa gga gtc aca act cta atg tct gat gac aca ggg cag gag	1008
Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu	
325 330 335	
att gag aag tct gac att cgc aag gca tac aag ttt ggt ggc gag cag	1056
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Glu Gln	
340 345 350	
gta tca ttc acc atc gaa gaa caa cag gcg cta aga agc ttc ggt gac	1104
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp	
355 360 365	
ccg gtg atc cgt att att ggg ttc aag cca ctg tca gcc ctc ccg ttc	1152
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe	
370 375 380	
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Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp	
385 390 395 400	
tac gtc ggt tca aca aga gtc ttt tct gca ctg cat cag aaa ctc ctc	1248
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu	
405 410 415	
gaa tcg gag aaa ctg gct ttg gtc tgg ttc atc ccc cgc aga aat gcc	1296
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala	
420 425 430	

tca cca gtc tta gct gct atg att gca ggt gct gag aag atc gac gag	1344
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu	
435 440 445	
aat ggc gtg cag aaa att cca cct ggg atg tgg att atc cct ctt cct	1392
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro	
450 455 460	
ttc gca gat gat gtg cgc caa aat cca gag agc acc gtc cac cgg gca	1440
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala	
465 470 475 480	
gga gat gcg ctg aac gac gcc atg cga gat gtt gtt cgc cag ttg cag	1488
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln	
485 490 495	
ctc ccc aag gct gtg tac gat cct tca aaa tat ccg aat cct tcg ctt	1536
Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu	
500 505 510	
caa tgg cat tat cgt atc tta cag gct atc gcc ttg gat gaa gat ttc	1584
Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe	
515 520 525	
cca gaa tca cca gat gac aag acc gtg cct aag tac cga cag gtt cac	1632
Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His	
530 535 540	
aag gtt ggc tgc ttc cat gat ccc aga aat gcc cga aca tgg gcc gag	1680
Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu	
545 550 555 560	
gaa ctg aaa ttg caa gcc tcc gag atg ttt ggt ggg tca gta gcc gcc	1728
Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala	
565 570 575	
acc tct acg ctg gta aag cga ggt gcc aag acc gag gca gct ggt gag	1776
Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu	
580 585 590	
cac cca tca aag cgg gtg aag gtt gaa gac agt gag ccc gga gtg gaa	1824
His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu	
595 600 605	
gac gaa gtg aag aaa tgc tat gcg aaa ggc act gtt tcc aag ctt acg	1872
Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr	
610 615 620	
gtg gcc gtg ctg aag gaa ttc ttg cat gca cat ggc cgt gct aca gca	1920
Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala	
625 630 635 640	
gga aag aaa gca gat ctc gtg gac cga gtt gag cag tac ttt gag cag	1968
Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln	
645 650 655	
aag ttt taa	1977
Lys Phe	

<210> 20
 <211> 658
 <212> PRT
 <213> *Penicillium chrysogenum*

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 20 25 30

Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
35 40 45
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
50 55 60
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65 70 75 80
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
85 90 95
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
100 105 110
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
115 120 125
Leu Ala Ser Pro Ala Asp Ala Asp Asp Asp Val Leu Gln Val Leu Glu
130 135 140
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
145 150 155 160
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
165 170 175
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg
180 185 190
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
195 200 205
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser
210 215 220
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
225 230 235 240
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly
245 250 255
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg
260 265 270
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
275 280 285
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Lys Lys Gln
290 295 300
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Glu Thr Ala Gln
305 310 315 320
Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu
325 330 335
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln
340 345 350
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp
355 360 365
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe
370 375 380
Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp
385 390 395 400
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu
405 410 415
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala
420 425 430
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
435 440 445
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
450 455 460
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala
465 470 475 480
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln

<210> 21
<211> 3605
<212> DNA
<213> *Penicillium chrysogenum*

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 tccacttcca aatagagggg gctggcttct aacgacgcac agaccaccaa acac caacaa 180
 agacggcgtg tgatgtcatg tgccttcgtg tttcggtcta aaccgcaagt ggaa atatca 240
 cgctctgcc tttgtcttg agccccaaag caactttgtc ttgccatttt ccca acatca 300
 tcatcattat ggcggagaaa gaggctacag tttacattgt agacatggg cggc ctatgg 360
 gcgagcgcca ccatggccgt cctatgacag atctcgaatg ggcattgcag tatgtctggg 420
 ataggatcac tgccacggta tgtgacttga ccttgttcaa cgccagagaa ctga caattc 480
 caggtggcta ctggtcgaaa gacggctacg gttggcgttag ttggactcag gact gatgg 540
 gagtggtcgg ctaccagtca gcaccatttgc ggacccttgt ctcatgtttg gaac aggaac 600
 tatcaacgac ttggaaagaag agagctttc taatatttct attctcttcg gtct tggcca 660
 gtatgtgtgg cttaattaaat cgacagctt atgcccagtc gcctgactaa attgtctttc 720
 agagtcctca tgcctgataat ccggaaactg cgagaaacga tcaagcccag caac actaac 780
 agaggcgatg gtatgtgact gttgaagtct tgtcaagctg cttattctga cttt atataa 840
 gccatctttt ctattgtcat tgccatgcag atgatcatttgc actacacgaa gaaa aacaaa 900
 tacaagcgca agatcatctt ggtgaccaat ggtaccggcg tgatgagcga tgat aatatc 960
 gaaggcatca ttgaaaagat gaaagagggtt aacattgagt tggtggtcat gtat gtttct 1020
 tgccgacatg acttcacatt catgctaata ctatgcagtg gagccgatt tgat gacgct 1080
 gagtatggtg taaaggaaga agacaaagac agtcgaaagg ttctaagcca tctc caatct 1140
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 cctggctgag gactgcgaag gtgcttatgg aacgctggag caagccgttt cggaaattggaa 1260
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 caatccccgag gagtatgaca cggctatgac tataccctgtg gagcgatact tccgaaaccta 1380
 cgtcgccaaa ccaatctcag cgagctcggt cgtaccacgc tccggcacccg aacc tggaag 1440
 tcaagcaccg gttaaaggcg atgctgaagg cgatgctctc gcctcagtgc gaac atcacg 1500
 gacgtatcag atcacagatg agtccgcacc aggtggtaag atcgacgttg aacg cgatga 1560
 cctcqccaaq qqqtacqagt acqqqacqtaq cqcqqtctt atcqqaqcaaa ccqatgagaa 1620

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gttcccacct	ttggataaga	ttatcactgt	ctctggcaag	gtggtgactg	aacatcgaaa	2040
cctcccaaggc	gtggcgttga	aagatgcgt	gagtaactac	gtggacagca	tggattttgt	2100
caccacaaac	gacgaagggt	aagtatagtc	tacttgatta	tcgactttat	cagttaatca	2160
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ctgctcagcc	tcgaacccaa	gcgaacgaag	atttccaccg	agaatgcaat	cccagagttc	2580
aagcaaacac	tttcccgcc	ggaaaacatc	gacgcaatcc	acgacgctgt	gcagcagatg	2640
gctaaaatca	tccggagcc	gatcacacac	agcctcggtc	attcaaatta	cgaccgtgtt	2700
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gggtccaaataa	tactgaccac	ccagatcaa	ggatacggat	tggagggtt	acggagaaat	3240
ggaaatattt	agcaagccca	tgaacagcat	tgtcatatag	acgtagaatt	gacacataca	3300
ggAACGAAGC	ccgcagacag	aacaatatga	ggcacaa	gaatcggtgc	ccaattgca	3360
ggcatgacga	gtcgtcaatg	aacaacagaa	ccaaacgccc	tgcataacat	gcccaataac	3420
cagtattcgc	tccagaaaac	agcaaaaagac	cgagatttgc	aaactcaaac	attaaaaagc	3480
atccagatgc	atcagggaaa	aggggtatgc	agaagtgtt	tcccggtagg	acgagaagaa	3540
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aacat						3605

<210> 22

<211> 2157

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1)..(2157)

<400> 22

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Met	Ala	Glu	Lys	Glu	Ala	Thr	Val	Tyr	Ile	Val	Asp	Met	Gly	Arg	Ser

1				5				10				15			
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atg	ggc	gag	cg	cac	cat	ggc	cgt	cct	atg	aca	gat	ctc	gaa	tgg	gcc
Met	Gly	Gl	Arg	His	His	Gly	Arg	Pro	Met	Thr	Asp	Leu	Glu	Trp	Ala

20				25				30							
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atg	cag	tat	gtc	tgg	gat	agg	atc	act	gcc	acg	gtg	gct	act	ggt	cga
Met	Gln	Tyr	Val	Trp	Asp	Arg	Ile	Thr	Ala	Thr	Val	Ala	Thr	Gly	Arg

35				40				45							
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aag	acg	gct	acg	gtt	ggc	gta	gtt	gga	ctc	agg	act	gat	gtc	acg	acc
Lys	Thr	Ala	Thr	Val	Gly	Val	Val	Gly	Leu	Arg	Thr	Asp	Val	Ser	Thr

48

96

144

192

50	55	60	
cat tgg gac cct tgt ctc atg ttt gga aca gga act atc aac gac tttg			240
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu			
65	70	75	80
gaa gaa gag agc ttt tct aat att tct att ctc ttc ggt ctt ggc Caa			288
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln			
85	90	95	
gtc ctc atg cct gat atc cgg aaa ctg cga gaa acg atc aag ccc agc			336
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser			
100	105	110	
aac act aac aga ggc gat gcc atc tct tct att gtc att gcc atg Cag			384
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln			
115	120	125	
atg atc att gac tac acg aag aaa aac aaa tac aag cgc aag atc atc			432
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile			
130	135	140	
ttg gtg acc aat ggt acc ggc gtg atg agc gat gat aat atc gaa ggc			480
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly			
145	150	155	160
atc att gaa aag atg aaa gag gtt aac att gag ttg gtg gtc atg tat			528
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr			
165	170	175	
tat ggt gta aag gaa gaa gac aaa gac agt cga aag gct gaa aac gag			576
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu			
180	185	190	
act ttt ctc cga agc ctg gct gag gac tgc gaa ggt gct tat gga agc			624
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr			
195	200	205	
ctg gag caa gcc gtt tcg gaa ttg gat att ccc cgt atc aaa gtg acc			672
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr			
210	215	220	
aag agc atg cca tct ttc aag gga aac ctc acg ctc ggc aat ccc gag			720
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu			
225	230	235	240
gag tat gac acg gct atg act ata ccc gtg gag cga tac ttc cga acc			768
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr			
245	250	255	
tac gtc gcc aaa cca atc tca gcg agc tcg ttc gta cca cgc tcc ggc			816
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly			
260	265	270	
acc gaa cct gga agt caa gca ccg gtt aaa ggc gat gct gaa ggc gat			864
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp			
275	280	285	
gct ctc gcc tca gtg cga aca tca cgg acg tat cag atc aca gat gag			912
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu			
290	295	300	
tcc gca cca ggt ggt aag atc gac gtt gaa cgc gat gac ctc gcc aga			960
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys			
305	310	315	320
ggg tac gag tac gga cgt acc gcg gtt cct atc gag caa acc gat gag			1008
Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu			
325	330	335	
aat gtt gca aat cta caa aca ttt gct ggt atg ggg ctg atc ggg ttc			1056
Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe			
340	345	350	
gtt cag aag gat cag tat gac cgg tac atg cat atg tca aac acg aat			1104
Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn			

355	360	365	
atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct			1152
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser			
370	375	380	
tct ctc att cat gca ctc tac gaa ttg gag tcc tat gcg gtt gcc Cgc			1200
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg			
385	390	395	400
ttg gtg acc aaa gaa tcc aaa cca ccg atg ctt gtg ttg cta gct Cca			1248
Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro			
405	410	415	
tct atc gag gca gac tat gag tgc ttg att gaa gta cag ctt cca ttt			1296
Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe			
420	425	430	
gca gaa gac gtg cgg tcg tat cgg ttc cca cct ttg gat aag att atc			1344
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile			
435	440	445	
act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc Gtg			1392
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val			
450	455	460	
gcg ttg aaa gat gcg atg agt aac tac gtg gac agc atg gat ttt Gtc			1440
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val			
465	470	475	480
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag			1488
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu			
485	490	495	
tca ttc tca ccg tta ttg cac cgc atc gaa tca gca gtt cga tat Cgt			1536
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg			
500	505	510	
gct gtg cat ccc aat gac cct gtc ctc gac ccc tca gag cgg ctc act			1584
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr			
515	520	525	
gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc Cat			1632
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His			
530	535	540	
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag			1680
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys			
545	550	555	560
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca Ggt			1728
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly			
565	570	575	
ttg gac gtg gac gcc ctg ctc agc ctc gaa ccc aag cga acg aag att			1776
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile			
580	585	590	
tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc Gcg			1824
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala			
595	600	605	
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc			1872
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile			
610	615	620	
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac Cgt			1920
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg			
625	630	635	640
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag			1968
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu			
645	650	655	
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg			2016
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met			

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<211> 718
<212> PRT
<213> *Penicillium chrysogenum*

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 Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
 35 40 45
 Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr
 50 55 60
 His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu
 65 70 75 80
 Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln
 85 90 95
 Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser
 100 105 110
 Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln
 115 120 125
 Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile
 130 135 140
 Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly
 145 150 155 160
 Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr
 165 170 175
 Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu
 180 185 190
 Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr
 195 200 205
 Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr
 210 215 220
 Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
 225 230 235 240
 Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
 245 250 255
 Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
 260 265 270
 Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
 275 280 285
 Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
 290 295 300
 Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys

305 310 315 320
Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
 325 330 335
Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
 340 345 350
Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
 355 360 365
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
 370 375 380
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
 385 390 395 400
Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
 405 410 415
Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
 420 425 430
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
 435 440 445
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
 450 455 460
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
 465 470 475 480
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
 485 490 495
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
 500 505 510
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
 515 520 525
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His
 530 535 540
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys
 545 550 555 560
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly
 565 570 575
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile
 580 585 590
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala
 595 600 605
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile
 610 615 620
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg
 625 630 635 640
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu
 645 650 655
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met
 660 665 670
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val
 675 680 685
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
 690 695 700
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn
 705 710 715